

0270

OIPE

RAW SEQUENCE LISTING

DATE: 10/20/2000

PATENT APPLICATION: US/09/686,346

TIME: 10:57:18

Input Set: A:\421C1.App

Output Set: N:\CRF3\10202000\I686346.raw

4 <110> APPLICANT: Cobb, Melanie
5 Hutchison, Michele
6 Chen, Zhu
7 Berman, Kevin
9 <120> TITLE OF INVENTION: TAO PROTEIN KINASE POLYPEPTIDES AND
10 METHODS OF USE THEREFOR
12 <130> FILE REFERENCE: 860098.421C1
C--> 14 <140> CURRENT APPLICATION NUMBER: US/09/686,346
C--> 14 <141> CURRENT FILING DATE: 2000-10-10
14 <150> PRIOR APPLICATION NUMBER: 09/060,410
15 <151> PRIOR FILING DATE: 1998-04-14
17 <160> NUMBER OF SEQ ID NOS: 28
19 <170> SOFTWARE: FastSEQ for Windows Version 4.0
21 <210> SEQ ID NO: 1
22 <211> LENGTH: 3312
23 <212> TYPE: DNA
24 <213> ORGANISM: Rattus norvegicus
26 <220> FEATURE:
27 <221> NAME/KEY: CDS
28 <222> LOCATION: (121)...(3123)
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32 tgaaccaagc tttgggatag cagtataaaa ttagaatcag acagctgact gctcagcagg 120
33 atg cca tca act aac aga gca ggc agt cta aag gac cct gaa atc gca 168
34 Met Pro Ser Thr Asn Arg Ala Gly Ser Leu Lys Asp Pro Glu Ile Ala
35 1 5 10 15
37 gag ctc ttc ttc aaa gaa gat ccg gaa aaa ctc ttc aca gat ctc aga 216
38 Glu Leu Phe Phe Lys Glu Asp Pro Glu Lys Leu Phe Thr Asp Leu Arg
39 20 25 30
41 gaa atc ggc cat ggg agc ttt gga gca gtt tat ttt gca cga gat gtg 264
42 Glu Ile Gly His Gly Ser Phe Gly Ala Val Tyr Phe Ala Arg Asp Val
43 35 40 45
45 cgt act aat gaa gtg gtg gcc atc aag aaa atg tct tat agt gga aag 312
46 Arg Thr Asn Glu Val Val Ala Ile Lys Lys Met Ser Tyr Ser Gly Lys
47 50 55 60
49 cag tct act gag aaa tgg cag gat att att aag gaa gtc aag ttt cta 360
50 Gln Ser Thr Glu Lys Trp Gln Asp Ile Ile Lys Glu Val Lys Phe Leu
51 65 70 75 80
53 caa aga ata aaa cat ccc aac agt ata gaa tac aaa ggc tgc tat tta 408
54 Gln Arg Ile Lys His Pro Asn Ser Ile Glu Tyr Lys Gly Cys Tyr Leu
55 85 90 95
57 cgt gaa cac aca gca tgg ctt gta atg gaa tat tgt tta gga tct gct 456
58 Arg Glu His Thr Ala Trp Leu Val Met Glu Tyr Cys Leu Gly Ser Ala
59 100 105 110
61 tcg gat tta cta gaa gtt cat aaa aag cca tta caa gaa gtg gaa ata 504
62 Ser Asp Leu Leu Glu Val His Lys Lys Pro Leu Gln Glu Val Glu Ile
63 115 120 125

ENTERED

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65 gca gca att aca cat ggt gct ctc cag gga tta gct tat tta cat tct 552
66 Ala Ala Ile Thr His Gly Ala Leu Gln Gly Leu Ala Tyr Leu His Ser
67 130 135 140
69 cat acc atg atc cat aga gat atc aaa gca gga aat atc ctt ctg aca 600
70 His Thr Met Ile His Arg Asp Ile Lys Ala Gly Asn Ile Leu Leu Thr
71 145 150 155 160
73 gaa cca ggc caa gtg aaa ctt gct gac ttt gga tct gct tcc atg gcc 648
74 Glu Pro Gly Gln Val Lys Leu Ala Asp Phe Gly Ser Ala Ser Met Ala
75 165 170 175
77 tcc cct gcc aat tct ttt gtg gga aca cca tat tgg atg gcc cca gaa 696
78 Ser Pro Ala Asn Ser Phe Val Gly Thr Pro Tyr Trp Met Ala Pro Glu
79 180 185 190
81 gta att tta gcc atg gat gaa gga caa tat gat ggc aaa gtt gat gta 744
82 Val Ile Leu Ala Met Asp Glu Gly Gln Tyr Asp Gly Lys Val Asp Val
83 195 200 205
85 tgg tct ctt gga ata aca tgt att gaa tta gcc gag agg aag cct cct 792
86 Trp Ser Leu Gly Ile Thr Cys Ile Glu Leu Ala Glu Arg Lys Pro Pro
87 210 215 220
89 tta ttt aat atg aat gca atg agt gcc tta tat cac ata gcc caa aat 840
90 Leu Phe Asn Met Asn Ala Met Ser Ala Leu Tyr His Ile Ala Gln Asn
91 225 230 235 240
93 gaa tcc cct aca cta cag tct aat gaa tgg tct gat tat ttt cga aac 888
94 Glu Ser Pro Thr Leu Gln Ser Asn Glu Trp Ser Asp Tyr Phe Arg Asn
95 245 250 255
97 ttt gta gat tct tgc ctc cag aaa atc cct caa gat cgc cct aca tca 936
98 Phe Val Asp Ser Cys Leu Gln Lys Ile Pro Gln Asp Arg Pro Thr Ser
99 260 265 270
101 gag gaa ctt tta aag cac atg ttt gtt ctt cga gag cgc cct gaa aca 984
102 Glu Glu Leu Leu Lys His Met Phe Val Leu Arg Glu Arg Pro Glu Thr
103 275 280 285
105 gtg tta ata gat ctt att caa agg aca aag gat gca gta aga gag ctg 1032
106 Val Leu Ile Asp Leu Ile Gln Arg Thr Lys Asp Ala Val Arg Glu Leu
107 290 295 300
109 gac aat cta caa tat cga aag atg aag aaa ctc ctt ttc cag gag gca 1080
110 Asp Asn Leu Gln Tyr Arg Lys Met Lys Lys Leu Leu Phe Gln Glu Ala
111 305 310 315 320
113 cat aat gga cca gca gta gaa gca cag gaa gaa gag gag gag caa gat 1128
114 His Asn Gly Pro Ala Val Glu Ala Gln Glu Glu Glu Glu Gln Asp
115 325 330 335
117 cat ggt ggt ggc cgg aca gga aca gta aat agt gtt gga agc aat cag 1176
118 His Gly Gly Gly Arg Thr Gly Thr Val Asn Ser Val Gly Ser Asn Gln
119 340 345 350
121 tct atc ccc agt atg tct atc agt gcc agt agc caa agc agc agt gtt 1224
122 Ser Ile Pro Ser Met Ser Ile Ser Ala Ser Ser Gln Ser Ser Ser Val
123 355 360 365
125 aat agt ctt cca gat gca tgg gat gac aag agt gag cta gac atg atg 1272
126 Asn Ser Leu Pro Asp Ala Ser Asp Asp Lys Ser Glu Leu Asp Met Met
127 370 375 380
129 gag gga gac cat aca gtg atg tct aac agt tct gtc atc cac tta aaa 1320

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130	Glu	Gly	Asp	His	Thr	Val	Met	Ser	Asn	Ser	Ser	Val	Ile	His	Leu	Lys	
131	385					390						395				400	
133	cct	gag	gag	gaa	aat	tac	caa	gaa	gaa	gga	gat	cct	aga	aca	aga	gca	1368
134	Pro	Glu	Glu	Glu	Asn	Tyr	Gln	Glu	Glu	Gly	Asp	Pro	Arg	Thr	Arg	Ala	
135					405					410					415		
137	tca	gct	cca	cag	tct	cca	cct	caa	gtg	tct	cgt	cac	aaa	tca	cat	tat	1416
138	Ser	Ala	Pro	Gln	Ser	Pro	Pro	Gln	Val	Ser	Arg	His	Lys	Ser	His	Tyr	
139					420					425					430		
141	cgt	aat	aga	gaa	cac	ttt	gca	act	ata	cga	aca	gca	tca	ctg	gtt	aca	1464
142	Arg	Asn	Arg	Glu	His	Phe	Ala	Thr	Ile	Arg	Thr	Ala	Ser	Leu	Val	Thr	
143					435					440					445		
145	aga	cag	atg	caa	gaa	cat	gag	cag	gac	tct	gaa	ctt	aga	gaa	cag	atg	1512
146	Arg	Gln	Met	Gln	Glu	His	Glu	Gln	Asp	Ser	Glu	Leu	Arg	Glu	Gln	Met	
147		450						455				460					
149	tct	ggt	tat	aag	cgg	atg	agg	cga	cag	cat	cag	aag	cag	ctg	atg	act	1560
150	Ser	Gly	Tyr	Lys	Arg	Met	Arg	Arg	Gln	His	Gln	Lys	Gln	Leu	Met	Thr	
151	465					470					475					480	
153	ctg	gaa	aat	aaa	ctg	aag	gca	gaa	atg	gac	gaa	cat	cgg	ctc	aga	tta	1608
154	Leu	Glu	Asn	Lys	Leu	Lys	Ala	Glu	Met	Asp	Glu	His	Arg	Leu	Arg	Leu	
155					485						490				495		
157	gac	aaa	gat	ctt	gaa	act	cag	cgc	aac	aat	ttc	gct	gca	gaa	atg	gag	1656
158	Asp	Lys	Asp	Leu	Glu	Thr	Gln	Arg	Asn	Asn	Phe	Ala	Ala	Glu	Met	Glu	
159					500					505					510		
161	aaa	ctt	att	aag	aaa	cac	caa	gct	tct	atg	gaa	aaa	gag	gct	aaa	gtg	1704
162	Lys	Leu	Ile	Lys	Lys	His	Gln	Ala	Ser	Met	Glu	Lys	Glu	Ala	Lys	Val	
163					515					520					525		
165	atg	gcc	aac	gag	gag	aaa	aaa	ttc	caa	caa	cac	att	cag	gct	caa	cag	1752
166	Met	Ala	Asn	Glu	Glu	Lys	Lys	Phe	Gln	Gln	His	Ile	Gln	Ala	Gln	Gln	
167		530						535				540					
169	aag	aaa	gaa	ctg	aat	agc	ttt	ttg	gag	tct	caa	aaa	aga	gaa	tat	aaa	1800
170	Lys	Lys	Glu	Leu	Asn	Ser	Phe	Leu	Glu	Ser	Gln	Lys	Arg	Glu	Tyr	Lys	
171	545					550					555					560	
173	ctt	cga	aaa	gag	cag	ctt	aag	gag	gag	ctg	aat	gaa	aac	cag	agc	aca	1848
174	Leu	Arg	Lys	Glu	Gln	Leu	Lys	Glu	Glu	Leu	Asn	Glu	Asn	Gln	Ser	Thr	
175					565					570					575		
177	cct	aaa	aaa	gaa	aag	cag	gaa	tgg	ctt	tca	aag	cag	aag	gag	aat	att	1896
178	Pro	Lys	Lys	Glu	Lys	Gln	Glu	Trp	Leu	Ser	Lys	Gln	Lys	Glu	Asn	Ile	
179					580					585					590		
181	caa	cat	ttt	cag	gca	gaa	gaa	gaa	gct	aat	ctt	ctt	cga	cgt	caa	agg	1944
182	Gln	His	Phe	Gln	Ala	Glu	Glu	Glu	Ala	Asn	Leu	Leu	Arg	Arg	Gln	Arg	
183					595				600					605			
185	cag	tat	cta	gag	cta	gaa	tgt	cgt	cgc	ttc	aaa	aga	aga	atg	tta	ctt	1992
186	Gln	Tyr	Leu	Glu	Leu	Glu	Cys	Arg	Arg	Phe	Lys	Arg	Arg	Met	Leu	Leu	
187		610					615					620					
189	ggt	cgg	cat	aac	ttg	gaa	cag	gac	ctt	gtc	agg	gag	gag	tta	aac	aaa	2040
190	Gly	Arg	His	Asn	Leu	Glu	Gln	Asp	Leu	Val	Arg	Glu	Glu	Leu	Asn	Lys	
191	625					630					635					640	
193	agg	cag	act	cag	aag	gac	tta	gaa	cat	gca	atg	tta	ctg	cga	cag	cat	2088
194	Arg	Gln	Thr	Gln	Lys	Asp	Leu	Glu	His	Ala	Met	Leu	Leu	Arg	Gln	His	

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195																645																650																655																																
197	gaa	tcc	atg	caa	gaa	ctg	gag	ttt	cgc	cac	ctc	aac	act	att	cag	aag		2136																																																														
198	Glu	Ser	Met	Gln	Glu	Leu	Glu	Phe	Arg	His	Leu	Asn	Thr	Ile	Gln	Lys																																																																
199																660																665																670																																
201	atg	cgc	tgt	gag	ttg	atc	aga	ctg	caa	cat	caa	act	gag	ctt	act	aac		2184																																																														
202	Met	Arg	Cys	Glu	Leu	Ile	Arg	Leu	Gln	His	Gln	Thr	Glu	Leu	Thr	Asn																																																																
203																675																680																685																																
205	cag	ctg	gaa	tac	aat	aag	aga	agg	gaa	cgg	gaa	cta	aga	cgg	aaa	cat		2232																																																														
206	Gln	Leu	Glu	Tyr	Asn	Lys	Arg	Arg	Glu	Arg	Glu	Leu	Arg	Arg	Lys	His																																																																
207																690																695																700																																
209	gtc	atg	gaa	gtt	cga	cag	cag	cct	aag	agt	ttg	aag	tct	aaa	gaa	ctc		2280																																																														
210	Val	Met	Glu	Val	Arg	Gln	Gln	Pro	Lys	Ser	Leu	Lys	Ser	Lys	Glu	Leu																																																																
211																705																710																715																720																
213	caa	ata	aaa	aag	cag	ttt	cag	gat	acc	tgc	aaa	att	caa	acc	aga	cag		2328																																																														
214	Gln	Ile	Lys	Lys	Gln	Phe	Gln	Asp	Thr	Cys	Lys	Ile	Gln	Thr	Arg	Gln																																																																
215																725																730																735																																
217	tac	aaa	gca	tta	agg	aat	cac	cta	ctg	gag	act	aca	cca	aag	agt	gag		2376																																																														
218	Tyr	Lys	Ala	Leu	Arg	Asn	His	Leu	Leu	Glu	Thr	Thr	Pro	Lys	Ser	Glu																																																																
219																740																745																750																																
221	cac	aaa	gct	gtt	ctg	aaa	aga	ctc	aag	gag	gaa	cag	act	cgg	aag	tta		2424																																																														
222	His	Lys	Ala	Val	Leu	Lys	Arg	Leu	Lys	Glu	Glu	Gln	Thr	Arg	Lys	Leu																																																																
223																755																760																765																																
225	gcc	atc	ttg	gct	gag	cag	tat	gat	cat	agc	att	aat	gaa	atg	ctc	tcc		2472																																																														
226	Ala	Ile	Leu	Ala	Glu	Gln	Tyr	Asp	His	Ser	Ile	Asn	Glu	Met	Leu	Ser																																																																
227																770																775																780																																
229	aca	caa	gct	ctg	cgt	ttg	gat	gaa	gca	cag	gaa	gca	gaa	tgc	cag	gtt		2520																																																														
230	Thr	Gln	Ala	Leu	Arg	Leu	Asp	Glu	Ala	Gln	Glu	Ala	Glu	Cys	Gln	Val																																																																
231																785																790																795																800																
233	ttg	aag	atg	cag	cta	cag	cag	gaa	ctg	gag	ctg	ttg	aat	gca	tat	cag		2568																																																														
234	Leu	Lys	Met	Gln	Gln	Gln	Glu	Leu	Glu	Leu	Leu	Leu	Asn	Ala	Tyr	Gln																																																																
235																805																810																815																																
237	agc	aaa	atc	aag	atg	cag	gct	gag	gcc	caa	cat	gat	cga	gag	ctt	cga		2616																																																														
238	Ser	Lys	Ile	Lys	Met	Gln	Ala	Glu	Ala	Gln	His	Asp	Arg	Glu	Leu	Arg																																																																
239																820																825																830																																
241	gag	ctg	gaa	caa	agg	gtc	tcc	ctt	cgg	aga	gca	ctc	tta	gaa	cag	aag		2664																																																														
242	Glu	Leu	Glu	Gln	Arg	Val	Ser	Leu	Arg	Arg	Ala	Leu	Leu	Glu	Gln	Lys																																																																
243																835																840																845																																
245	att	gaa	gaa	gag	atg	ttg	gct	ttg	cag	aat	gaa	cgc	aca	gaa	cga	ata		2712																																																														
246	Ile	Glu	Glu</																																																																													

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261 aat cct act ggg ggt tca gga cct cac tgg ggt cat ccc atg ggt ggc 2904
262 Asn Pro Thr Gly Gly Ser Gly Pro His Trp Gly His Pro Met Gly Gly
263 915 920 925
265 aca cca caa gct tgg ggt cat ccg atg caa ggc gga ccc caa cca tgg 2952
266 Thr Pro Gln Ala Trp Gly His Pro Met Gln Gly Gly Pro Gln Pro Trp
267 930 935 940
269 ggt cac ccc tca ggg cca atg caa ggg gta cct cga ggt agc agt ata 3000
270 Gly His Pro Ser Gly Pro Met Gln Gly Val Pro Arg Gly Ser Ser Ile
271 945 950 955 960
273 gga gtc cgc aat agc ccc cag gct ctg agg cgg aca gct tct ggg gga 3048
274 Gly Val Arg Asn Ser Pro Gln Ala Leu Arg Arg Thr Ala Ser Gly Gly
275 965 970 975
277 cgg acg gaa cag ggc atg agc aga agc acg agt gtc act tca caa ata 3096
278 Arg Thr Glu Gln Gly Met Ser Arg Ser Thr Ser Val Thr Ser Gln Ile
279 980 985 990
281 tcc aat ggg tca cac atg tct tac aca taataattga aagtggcaat 3143
282 Ser Asn Gly Ser His Met Ser Tyr Thr
283 995 1000
285 tccgctggag ctgtctgccaa aaagaaactg cctacagaca tcagcacagc agcctcctca 3203
286 ctggggtact accgggtgga agctgtgcat atggtatatt ttattcgtct ttgtaaagcg 3263
287 ttatgttttg tgtttactaa ttgggatgtc atagtatttg gctgcggg 3312
289 <210> SEQ ID NO: 2
290 <211> LENGTH: 1001
291 <212> TYPE: PRT
292 <213> ORGANISM: Rattus norvegicus
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296 1 5 10 15
297 Glu Leu Phe Phe Lys Glu Asp Pro Glu Lys Leu Phe Thr Asp Leu Arg
298 20 25 30
299 Glu Ile Gly His Gly Ser Phe Gly Ala Val Tyr Phe Ala Arg Asp Val
300 35 40 45
301 Arg Thr Asn Glu Val Val Ala Ile Lys Lys Met Ser Tyr Ser Gly Lys
302 50 55 60
303 Gln Ser Thr Glu Lys Trp Gln Asp Ile Ile Lys Glu Val Lys Phe Leu
304 65 70 75 80
305 Gln Arg Ile Lys His Pro Asn Ser Ile Glu Tyr Lys Gly Cys Tyr Leu
306 85 90 95
307 Arg Glu His Thr Ala Trp Leu Val Met Glu Tyr Cys Leu Gly Ser Ala
308 100 105 110
309 Ser Asp Leu Leu Glu Val His Lys Lys Pro Leu Gln Glu Val Glu Ile
310 115 120 125
311 Ala Ala Ile Thr His Gly Ala Leu Gln Gly Leu Ala Tyr Leu His Ser
312 130 135 140
313 His Thr Met Ile His Arg Asp Ile Lys Ala Gly Asn Ile Leu Leu Thr
314 145 150 155 160
315 Glu Pro Gly Gln Val Lys Leu Ala Asp Phe Gly Ser Ala Ser Met Ala
316 165 170 175
317 Ser Pro Ala Asn Ser Phe Val Gly Thr Pro Tyr Trp Met Ala Pro Glu

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Please Note:

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

VERIFICATION SUMMARY

DATE: 10/20/2000

PATENT APPLICATION: US/09/686,346

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Input Set : A:\421C1.App

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L:14 M:270 C: Current Application Number differs, Replaced Current Application No
L:14 M:271 C: Current Filing Date differs, Replaced Current Filing Date
L:929 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:5
L:930 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:5
L:931 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:5
L:964 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:7
L:1003 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:10
L:1016 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:11
L:1163 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:19
L:1178 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:20
L:1193 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:21
L:1208 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:22